



SEQUENCE LISTING

RECEIVED  
AUG 29 2000  
TECH CENTER 1600-2000

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AUG 23 2000  
TECH CENTER 1600-2000

(1) GENERAL INFORMATION:

- (i) APPLICANT: LAFFEND, LISA ANNE  
NAGARAJAN, VASANTHA  
NAKAMURA, CHARLES
- (ii) TITLE OF INVENTION: BIOCONVERSION OF A FERMENTABLE  
CARBON SOURCE TO 1,3-PROPANE-  
DIOL BY A SINGLE MICROORGANISM
- (iii) NUMBER OF SEQUENCES: 46
- (iv) CORRESPONDENCE ADDRESS:
  - (A) NAME: E. I. DUPONT DE NEMOURS AND COMPANY
  - (B) STREET: 1007 MARKET STREET
  - (C) CITY: WILMINGTON
  - (D) STATE: DELAWARE
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 19898
- (iv) CORRESPONDENCE ADDRESS:
  - (A) NAME: GENENCOR INTERNATIONAL, INC.
  - (B) STREET: 4 CAMBRIDGE PLACE  
1870 SOUTH WINTON ROAD
  - (C) CITY: ROCHESTER
  - (D) STATE: NEW YORK
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 14618
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.50 INCH DISKETTE
  - (B) COMPUTER: IBM
  - (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
  - (D) SOFTWARE: MICROSOFT WORD 7.0A
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/440,293
  - (B) FILING DATE: MAY 12, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: LINDA AXAMETHY FLOYD
  - (B) REGISTRATION NUMBER: 33,692
  - (C) REFERENCE/DOCKET NUMBER: CR9715 US DIV1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 302-892-8112
  - (B) TELEFAX: 302-773-0164

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12145 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACCACC ACGGTGGTGA CTTTAATGCC GCTCTCATGC AGCAGCTCGG TGGCGGTCTC 60  
AAAATTCAGG ATGTCGCCGG TATAGTTTTT GATAATCAGC AAGACGCCTT CGCCGCCGTC 120  
AATTTGCATC GCGCATTCAA ACATTTTGTC CGGCGTCGGC GAGGTGAATA TTTCCCCCGG 180  
ACAGGCGCCG GAGAGCATGC CCTGGCCGAT ATAGCCGCAG TGCATCGGTT CATGTCCGCT 240  
GCCGCCGCCG GAGAGCAGGG CCACCTTGCC AGCCACCGGC GCGTCGGTGC GGGTCACATA 300  
CAGCGGGTCC TGATGCAGGG TCAGCTGCGG ATGGGCTTTA GCCAGCCCCT GTAATTGTTC 360  
ATTCAGTACA TCTTCAACAC GGTTAATCAG CTTTTTCATT ATTCAGTGCT CCGTTGGAGA 420  
AGGTTTCGATG CCGCCTCTCT GCTGGCGGAG GCGGTCATCG CGTAGGGGTA TCGTCTGACG 480  
GTGGAGCGTG CCTGGCGATA TGATGATTCT GGCTGAGCGG ACGAAAAAAA GAATGCCCCG 540  
ACGATCGGGT TTCATTACGA AACATTGCTT CCTGATTTTG TTTCTTTATG GAACGTTTTT 600  
GCTGAGGATA TGGTGAAAAT GCGAGCTGGC GCGCTTTTTT TCTTCTGCCA TAAGCGGCGG 660  
TCAGGATAGC CGGCGAAGCG GGTGGGAAAA AATTTTTTGC TGATTTTCTG CCGACTGCGG 720  
GAGAAAAGGC GGTCAAACAC GGAGGATTGT AAGGGCATTG TCGGGCAAAG GAGCGGATCG 780  
GGATCGCAAT CCTGACAGAG ACTAGGGTTT TTTGTTCCAA TATGGAACGT AAAAAATTAA 840  
CCTGTGTTTC ATATCAGAAC AAAAAGGCGA AAGATTTTTT TGTTCCCTGC CGGCCCTACA 900  
GTGATCGCAC TGCTCCGGTA CGCTCCGTTC AGGCCGCGCT TCACTGGCCG GCGCGGATAA 960  
CGCCAGGGCT CATCATGTCT ACATGCGCAC TTATTTGAGG GTGAAAGGAA TGCTAAAAGT 1020  
TATTCAATCT CCAGCCAAAT ATCTTCAGGG TCCTGATGCT GCTGTTCTGT TCGGTCAATA 1080  
TGCCAAAAAC CTGGCGGAGA GCTTCTTCGT CATCGCTGAC GATTTTCGTAA TGAAGCTGGC 1140  
GGGAGAGAAA GTGGTGAATG GCCTGCAGAG CCACGATATT CGCTGCCATG CGGAACGGTT 1200  
TAACGGCGAA TGCAGCCATG CGGAAATCAA CCGTCTGATG GCGATTTTGC AAAACAGGG 1260  
CTGCCGCGGC GTGGTCGGGA TCGGCGGTGG TAAAACCCTC GATACCGCGA AGGCGATCGG 1320  
TTACTACCAG AAGCTGCCGG TGGTGGTGAT CCCGACCATC GCCTCGACCG ATGCGCCAAC 1380

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|------------|------------|------------|------------|------------|-------------|------|
| CAGCGCGCTG | TCGGTGATCT | ACACCGAAGC | GGGCGAGTTT | GAAGAGTATC | TGATCTATCC  | 1440 |
| GAAAAACCCG | GATATGGTGG | TGATGGACAC | GGCGATTATC | GCCAAAGCGC | CGGTACGCCT  | 1500 |
| GCTGGTCTCC | GGCATGGGCG | ATGCGCTCTC | CACCTGGTTC | GAGGCCAAAG | CTTGCTACGA  | 1560 |
| TGCGCGCGCC | ACCAGCATGG | CCGGAGGACA | GTCCACCGAG | GCGGCGCTGA | GCCTCGCCCG  | 1620 |
| CCTGTGCTAT | GATACGCTGC | TGGCGGAGGG | CGAAAAGGCC | CGTCTGGCGG | CGCAGGCCGG  | 1680 |
| GGTAGTGACC | GAAGCGCTGG | AGCGCATCAT | CGAGGCGAAC | ACTTACCTCA | GCGGCATTGG  | 1740 |
| CTTTGAAAGC | AGTGGCCTGG | CCGCTGCCCC | TGCAATCCAC | AACGGTTTCA | CCATTCTTGA  | 1800 |
| AGAGTGCCAT | CACCTGTATC | ACGGTGAGAA | AGTGGCCTTC | GGTACCCTGG | CGCAGCTGGT  | 1860 |
| GCTGCAGAAC | AGCCCGATGG | ACGAGATTGA | AACGGTGACG | GGCTTCTGCC | AGCGCGTCGG  | 1920 |
| CCTGCCGGTG | ACGCTCGCGC | AGATGGGCGT | CAAAGAGGGG | ATCGACGAGA | AAATCGCCGC  | 1980 |
| GGTGGCGAAA | GCTACCTGCG | CGGAAGGGGA | AACCATCCAT | AATATGCCGT | TTGCGGTGAC  | 2040 |
| CCCGGAGAGC | GTCCATGCCG | CTATCCTCAC | CGCCGATCTG | TTAGGCCAGC | AGTGGCTGGC  | 2100 |
| GCGTTAATTC | GCGGTGGCTA | AACCGCTGGC | CCAGGTCAGC | GGTTTTTCTT | TCTCCCCTCC  | 2160 |
| GGCAGTCGCT | GCCGGAGGGG | TTCTCTATGG | TACAACGCGG | AAAAGGATAT | GA CTGTTCAG | 2220 |
| ACTCAGGATA | CCGGGAAGGC | GGTCTCTTCC | GTCATTGCCC | AGTCATGGCA | CCGCTGCAGC  | 2280 |
| AAGTTTATGC | AGCGCGAAAC | CTGGCAAACG | CCGCACCAGG | CCCAGGGCCT | GACCTTCGAC  | 2340 |
| TCCATCTGTC | GGCGTAAAAC | CGCGCTGCTC | ACCATCGGCC | AGGCGGCGCT | GGAAGACGCC  | 2400 |
| TGGGAGTTTA | TGGACGGCCG | CCCCTGCGCG | CTGTTTATTC | TTGATGAGTC | CGCCTGCATC  | 2460 |
| CTGAGCCGTT | GCGGCGAGCC | GCAAACCCTG | GCCCAGCTGG | CTGCCCTGGG | ATTTTCGCGAC | 2520 |
| GGCAGCTATT | GTGCGGAGAG | CATTATCGGC | ACCTGCGCGC | TGTCGCTGGC | CGCGATGCAG  | 2580 |
| GGCCAGCCGA | TCAACACCGC | CGGCGATCGG | CATTTTAAAG | AGGCGCTACA | GCCATGGAGT  | 2640 |
| TTTTGCTCGA | CGCCGGTGTT | TGATAACCAC | GGGCGGCTGT | TCGGCTCTAT | CTCGCTTTGC  | 2700 |
| TGTCTGGTCG | AGCACCAGTC | CAGCGCCGAC | CTCTCCCTGA | CGCTGGCCAT | CGCCCGCGAG  | 2760 |
| GTGGGTAACT | CCCTGCTTAC | CGACAGCCTG | CTGGCGGAAT | CCAACCGTCA | CCTCAATCAG  | 2820 |
| ATGTACGGCC | TGCTGGAGAG | CATGGACGAT | GGGGTGATGG | CGTGGAACGA | ACAGGGCGTG  | 2880 |
| CTGCAGTTTC | TCAATGTTCA | GGCGGCGAGA | CTGCTGCATC | TTGATGCTCA | GGCCAGCCAG  | 2940 |
| GGGAAAAATA | TCGCCGATCT | GGTGACCCTC | CCGGCGCTGC | TGCGCCGCGC | CATCAAACAC  | 3000 |
| GCCCGCGGCC | TGAATCACGT | CGAAGTCACC | TTTGAAAGTC | AGCATCAGTT | TGTCGATGCG  | 3060 |
| GTGATCACCT | TAAAACCGAT | TGTCGAGGCG | CAAGGCAACA | GTTTTATTCT | GCTGCTGCAT  | 3120 |

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| CCGGTGGAGC  | AGATGCGGCA | GCTGATGACC | AGCCAGCTCG  | GTAAAGTCAG | CCACACCTTT  | 3180 |
| GAGCAGATGT  | CTGCCGACGA | TCCGGAAACC | CGACGCCTGA  | TCCACTTTGG | CCGCCAGGCG  | 3240 |
| GCGCGCGGCG  | GCTTCCCGGT | GCTACTGTGC | GGCGAAGAGG  | GGGTCGGGAA | AGAGCTGCTG  | 3300 |
| AGCCAGGCTA  | TTCACAATGA | AAGCGAACGG | GCGGGCGGCC  | CCTACATCTC | CGTCAACTGC  | 3360 |
| CAGCTATATG  | CCGACAGCGT | GCTGGGCCAG | GACTTTATGG  | GCAGCGCCCC | TACCGACGAT  | 3420 |
| GAAAATGGTC  | GCCTGAGCCG | CCTTGAGCTG | GCCAACGGCG  | GCACCCTGTT | TCTGGAAAAG  | 3480 |
| ATCGAGTATC  | TGGCGCCGGA | GCTGCAGTCG | GCTCTGCTGC  | AGGTGATTAA | GCAGGGCGTG  | 3540 |
| CTCACCCGCC  | TCGACGCCCG | GCGCCTGATC | CCGGTGGATG  | TGAAGGTGAT | TGCCACCACC  | 3600 |
| ACCGTCGATC  | TGGCCAATCT | GGTGGAACAG | AACCGCTTTA  | GCCGCCAGCT | GTA CTATGCG | 3660 |
| CTGCACTCCT  | TTGAGATCGT | CATCCCGCCG | CTGCGCGCCC  | GACGCAACAG | TATTCCGTCG  | 3720 |
| CTGGTGCATA  | ACCGGTTGAA | GAGCCTGGAG | AAGCGTTTCT  | CTTCGCGACT | GAAAGTGGAC  | 3780 |
| GATGACGCGC  | TGGCACAGCT | GGTGGCCTAC | TCGTGGCCGG  | GGAATGATTT | TGAGCTCAAC  | 3840 |
| AGCGTCATTG  | AGAATATCGC | CATCAGCAGC | GACAACGGCC  | ACATTGCGCT | GAGTAATCTG  | 3900 |
| CCGGAATATC  | TCTTTTCCGA | GCGGCCGGGC | GGGGATAGCG  | CGTCATCGCT | GCTGCCGGCC  | 3960 |
| AGCCTGACTT  | TTAGCGCCAT | CGAAAAGGAA | GCTATTATTC  | ACGCCGCCCC | GGTGACCAGC  | 4020 |
| GGGCGGGTGC  | AGGAGATGTC | GCAGCTGCTC | AATATCGGCC  | GCACCACCCT | GTGGCGCAAA  | 4080 |
| ATGAAGCAGT  | ACGATATTGA | CGCCAGCCAG | TTCAAGCGCA  | AGCATCAGGC | CTAGTCTCTT  | 4140 |
| CGATTGCGCG  | CATGGAGAAC | AGGGCATCCG | ACAGGCGATT  | GCTGTAGCGT | TTGAGCGCGT  | 4200 |
| CGCGCAGCGG  | ATGCGCGCGG | TCCATGGCCG | TCAGCAGGCG  | TTGAGCCGA  | CGGGACTGGG  | 4260 |
| TGCGCGCCAC  | GTGCAGCTGG | GCAGAGGCGA | GATTCTCTCC  | CGGGATCACG | AACTGTTTTA  | 4320 |
| ACGGGCCGCT  | CTCGGCCATA | TTGCGGTGCA | TAAGCCGCTC  | CAGGGCGGTG | ATCTCCTCTT  | 4380 |
| CGCCGATCGT  | CTGGCTCAGG | CGGGTCAGGC | CCCGCGCATC  | GCTGGCCAGT | TCAGCCCCCA  | 4440 |
| GCACGAACAG  | CGTCTGCTGA | ATATGGTGCA | GGCTTTCCCG  | CAGCCCGGCG | TCGCGGGTCG  | 4500 |
| TGGCGTAGCA  | GACGCCCAGC | TGGGATATCA | GTTTCATCGAC | GGTGCCGTAG | GCCTCGACGC  | 4560 |
| GAATATGGTC  | TTTCTCGATG | CGGCTGCCGC | CGTACAGGGC  | GGTGGTGCCT | TTATCCCCGG  | 4620 |
| TGCGGGTATA  | GATACGATAC | ATTCAGTTTC | TCTCACTTAA  | CGGCAGGACT | TTAACCAGCT  | 4680 |
| GCCCCGCGTT  | GGCGCCGAGC | GTACGCAGTT | GATCGTCGCT  | ATCGGTGACG | TGTCCGGTAG  | 4740 |
| CCAGCGGCGC  | GTCCGCCGGC | AGCTGGGCAT | GAGTGAGGGC  | TATCTCGCCG | GACGCGCTGA  | 4800 |
| GCCCCGATACC | CACCCGCAGG | GGCGAGCTTC | TGGCCGCCAG  | GGCGCCGAGC | GCAGCGGCGT  | 4860 |

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| CACCGCCTCC | GTCATAGGTT | ATGGTCTGGC  | AGGGGACCCC  | CTGCTCCTCC | AGCCCCCAGC | 4920 |
| ACAGCTCATT | GATGGCGCCG | GCATGGTGCC  | CGCGCGGATC  | GTAAACAGG  | CGTACGCCTG | 4980 |
| GCGGTGAAAG | CGACATGACG | GTCCCCTCGT  | TAACACTCAG  | AATGCCTGGC | GGAAAATCGC | 5040 |
| GGCAATCTCC | TGCTCGTTGC | CTTTACGCGG  | GTTTCGAGAAC | GCATTGCCGT | CTTTTAGAGC | 5100 |
| CATCTCCGCC | ATGTAGGGGA | AGTCGGCCTC  | TTTTACCCCC  | AGATCGCGCA | GATGCTGCGG | 5160 |
| AATACCGATA | TCCATCGACA | GACGCGTGAT  | AGCGGCGATG  | GCTTTTTCGG | CCGCGTCGAG | 5220 |
| AGTGGACAGT | CCGGTGATAT | TTTCGCCCCAT | CAGTTCAGCG  | ATATCGGCGA | ATTTCTCCGG | 5280 |
| GTTGGCGATC | AGGTTGTAGC | GCGCCACATG  | CGGCAGCAGG  | ACAGCGTTGG | CCACGCCGTG | 5340 |
| CGGCATGTCG | TACAGGCCGC | CCAGCTGGTG  | CGCCATGGCG  | TGCACGTAGC | CGAGGTTGGC | 5400 |
| GTTATTGAAA | GCCATCCCGG | CCAGCAGAGA  | AGCATAGGCC  | ATGTTTTCCC | GCGCCTGCAG | 5460 |
| ATTGCTGCCG | AGGGCCACGG | CCTGGCGCAG  | GTTGCGGGCG  | ATGAGGCGGA | TCGCCTGCAT | 5520 |
| GGCGGCGGCG | TCCGTCACCG | GGTTAGCGTC  | TTTGAGATA   | TAGGCCTCTA | CGGCGTGGGT | 5580 |
| CAGGGCATCC | ATCCCGGTCG | CCGCGGTCAG  | GGCGGCCGGT  | TTACCGATCA | TCAGCAGTGG | 5640 |
| ATCGTTGATA | GAGACCGACG | GCAGTTTGCG  | CCAGCTGACG  | ATCACAAACT | TCACTTTGGT | 5700 |
| TTCGGTGTTG | GTCAGGACGC | AGTGGCGGGT  | GACCTCGCTG  | GCGGTGCCGG | CGGTGGTATT | 5760 |
| GACCGCGACG | ATAGGCGGCA | GCGGGTTGGT  | CAGGGTCTCG  | ATTCCGGCAT | ACTGGTACAG | 5820 |
| ATCGCCCTCA | TGGGTGGCGG | CGATGCCGAT  | GCCTTTGCCG  | CAATCGTGCG | GGCTGCCGCC | 5880 |
| GCCCACGGTG | ACGATGATGT | CGCACTGTTC  | GCGGCGAAAC  | ACGGCGAGGC | CGTCGCGCAC | 5940 |
| GTTGGTGTCT | TTCGGGTTCG | GCTCGACGCC  | GTCAAAGATC  | GCCACCTCGA | TCCCGGCCTC | 6000 |
| CCGCAGATAA | TGCAGGGTTT | TGTCCACCGC  | GCCATCTTTA  | ATTGCCCGCA | GGCCTTTGTC | 6060 |
| GGTGACCAGC | AGGGCTTTTT | TCCCCCCCAG  | CAGCTGGCAG  | CGTTCGCCGA | CTACGGAAAT | 6120 |
| GGCGTTGGGG | CCAAAAAGT  | TAACGTTTGG  | CACCAGATAA  | TCAAACATAC | GATAGCTCAT | 6180 |
| AATATACCTT | CTCGCTTCAG | GTTATAATGC  | GGAAAAACAA  | TCCAGGGCGC | ACTGGGCTAA | 6240 |
| TAATTGATCC | TGCTCGACCG | TACCGCCGCT  | AACGCCGACG  | GCGCCAATTA | CCTGCTCATT | 6300 |
| AAAAATAACT | GGCAGGCCGC | CGCCAAAAAT  | AATAATTCGC  | TGTTGGTTGG | TTAGCTGCAG | 6360 |
| ACCGTACAGA | GATTGTCCTG | GCTGGACCGC  | TGACGTAATT  | TCATGGGTAC | CTTGCTTCAG | 6420 |
| GCTGCAGGCG | CTCCAGGCTT | TATTCAGGGA  | AATATCGCAG  | CTGGAGACGA | AGGCCTCGTC | 6480 |
| CATCCGCTGG | ATAAGCAGCG | TGTTGCCTCC  | GCGGTCAACT  | ACGGAAAACA | CCACCGCCAC | 6540 |
| GTTGATCTCA | GTGGCTTTTT | TTTCCACCGC  | CGCCGCCATT  | TGCTGGGCGG | CGGCCAGGGT | 6600 |

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| GATTGTCTGA | ACTTGTTGGC | TCTTGTTTCAT | CATTCTCTCC | CGCACCAGGA | TAACGCTGGC | 6660 |
| GCGAATAGTC | AGTAGGGGGC | GATAGTAAAA  | AACTATTACC | ATTCGGTTGG | CTTGCTTTAT | 6720 |
| TTTTGTCAGC | GTTATTTTGT | CGCCCGCCAT  | GATTTAGTCA | ATAGGGTTAA | AATAGCGTCG | 6780 |
| GAAAAACGTA | ATTAAGGGCG | TTTTTTATTA  | ATTGATTTAT | ATCATTGCGG | GCGATCACAT | 6840 |
| TTTTTATTTT | TGCCGCCGGA | GTAAAGTTTC  | ATAGTGAAAC | TGTCGGTAGA | TTTCGTGTGC | 6900 |
| CAAATTGAAA | CGAAATTAAA | TTTATTTTTT  | TCACCACTGG | CTCATTTAAA | GTTCCGCTAT | 6960 |
| TGCCGGTAAT | GGCCGGGCGG | CAACGACGCT  | GGCCCGGCGT | ATTCGCTACC | GTCTGCGGAT | 7020 |
| TTCACCTTTT | GAGCCGATGA | ACAATGAAAA  | GATCAAAACG | ATTTGCAGTA | CTGGCCCAGC | 7080 |
| GCCCCGTCAA | TCAGGACGGG | CTGATTGGCG  | AGTGGCCTGA | AGAGGGGCTG | ATCGCCATGG | 7140 |
| ACAGCCCCTT | TGACCCGGTC | TCTTCAGTAA  | AAGTGGACAA | CGGTCTGATC | GTCGAACTGG | 7200 |
| ACGGCAAACG | CCGGGACCAG | TTTGACATGA  | TCGACCGATT | TATCGCCGAT | TACGCGATCA | 7260 |
| ACGTTGAGCG | CACAGAGCAG | GCAATGCGCC  | TGGAGGCGGT | GGAAATAGCC | CGTATGCTGG | 7320 |
| TGGATATTCA | CGTCAGCCGG | GAGGAGATCA  | TTGCCATCAC | TACCGCCATC | ACGCCGGCCA | 7380 |
| AAGCGGTCGA | GGTGATGGCG | CAGATGAACG  | TGGTGAGAT  | GATGATGGCG | CTGCAGAAGA | 7440 |
| TGCGTGCCCC | CCGGACCCCC | TCCAACCAGT  | GCCACGTCAC | CAATCTCAAA | GATAATCCGG | 7500 |
| TGCAGATTGC | CGCTGACGCC | GCCGAGGCCG  | GGATCCGCGG | CTTCTCAGAA | CAGGAGACCA | 7560 |
| CGGTCGGTAT | CGCGCGCTAC | GCGCCGTTTA  | ACGCCCTGGC | GCTGTTGGTC | GGTTGCGAGT | 7620 |
| GCGGCCGCCC | CGGCGTGTTG | ACGCAGTGCT  | CGGTGGAAGA | GGCCACCGAG | CTGGAGCTGG | 7680 |
| GCATGCGTGG | CTTAACCAGC | TACGCCGAGA  | CGGTGTCGGT | CTACGGCACC | GAAGCGGTAT | 7740 |
| TTACCGACGG | CGATGATACG | CCGTGGTCAA  | AGGCGTTCCT | CGCCTCGGCC | TACGCCTCCC | 7800 |
| GCGGGTTGAA | AATGCGCTAC | ACCTCCGGCA  | CCGGATCCGA | AGCGCTGATG | GGCTATTCGG | 7860 |
| AGAGCAAGTC | GATGCTCTAC | CTCGAATCGC  | GCTGCATCTT | CATTACTAAA | GGCGCCGGGG | 7920 |
| TTCAGGGACT | GCAAAACGGC | GCGGTGAGCT  | GATCGGCAT  | GACCGGCGCT | GTGCCGTCGG | 7980 |
| GCATTCGGGC | GGTGCTGGCG | GAAAACCTGA  | TCGCCTCTAT | GCTCGACCTC | GAAGTGGCGT | 8040 |
| CCGCCAACGA | CCAGACTTTC | TCCCACTCGG  | ATATTCGCCG | CACCGCGCGC | ACCCTGATGC | 8100 |
| AGATGCTGCC | GGGCACCGAC | TTTATTTTCT  | CCGGCTACAG | CGCGGTGCCG | AACTACGACA | 8160 |
| ACATGTTCGC | CGGCTCGAAC | TTCGATGCGG  | AAGATTTTGA | TGATTACAAC | ATCCTGCAGC | 8220 |
| GTGACCTGAT | GGTTGACGGC | GGCCTGCGTC  | CGGTGACCGA | GGCGGAAACC | ATTGCCATTC | 8280 |
| GCCAGAAAGC | GGCGCGGGCG | ATCCAGGCGG  | TTTTCCGCGA | GCTGGGGCTG | CCGCCAATCG | 8340 |

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| CCGACGAGGA | GGTGGAGGCC | GCCACCTACG | CGCACGGCAG | CAACGAGATG | CCGCCGCGTA | 8400  |
| ACGTGGTGGA | GGATCTGAGT | GCGGTGGAAG | AGATGATGAA | GCGCAACATC | ACCGGCCTCG | 8460  |
| ATATTGTCGG | CGCGCTGAGC | CGCAGCGGCT | TTGAGGATAT | CGCCAGCAAT | ATTCTCAATA | 8520  |
| TGCTGCGCCA | GCGGGTCACC | GGCGATTACC | TGCAGACCTC | GGCCATTCTC | GATCGGCAGT | 8580  |
| TCGAGGTGGT | GAGTGCGGTC | AACGACATCA | ATGACTATCA | GGGGCCGGGC | ACCGGCTATC | 8640  |
| GCATCTCTGC | CGAACGCTGG | GCGGAGATCA | AAAATATTCC | GGGCGTGGTT | CAGCCCGACA | 8700  |
| CCATTGAATA | AGGCGGTATT | CCTGTGCAAC | AGACAACCCA | AATTCAGCCC | TCTTTTACCC | 8760  |
| TGAAAACCCG | CGAGGGCGGG | GTAGCTTCTG | CCGATGAACG | CGCCGATGAA | GTGGTGATCG | 8820  |
| GCGTCGGCCC | TGCCTTCGAT | AAACACCAGC | ATCACACTCT | GATCGATATG | CCCCATGGCG | 8880  |
| CGATCCTCAA | AGAGCTGATT | GCCGGGGTGG | AAGAAGAGGG | GCTTCACGCC | CGGGTGGTGC | 8940  |
| GCATTCTGCG | CACGTCCGAC | GTCTCCTTTA | TGGCCTGGGA | TGCGGCCAAC | CTGAGCGGCT | 9000  |
| CGGGGATCGG | CATCGGTATC | CAGTCGAAGG | GGACCACGGT | CATCCATCAG | CGCGATCTGC | 9060  |
| TGCCGCTCAG | CAACCTGGAG | CTGTTCTCCC | AGGCGCCGCT | GCTGACGCTG | GAGACCTACC | 9120  |
| GGCAGATTGG | CAAAAACGCT | GCGCGCTATG | CGCGCAAAGA | GTCACCTTCG | CCGGTGCCGG | 9180  |
| TGGTGAACGA | TCAGATGGTG | CGGCCGAAAT | TTATGGCCAA | AGCCGCGCTA | TTTCATATCA | 9240  |
| AAGAGACCAA | ACATGTGGTG | CAGGACGCCG | AGCCCGTCAC | CCTGCACATC | GACTTAGTAA | 9300  |
| GGGAGTGACC | ATGAGCGAGA | AAACCATGCG | CGTGCAGGAT | TATCCGTTAG | CCACCCGCTG | 9360  |
| CCCGGAGCAT | ATCCTGACGC | CTACCGGCAA | ACCATTGACC | GATATTACCC | TCGAGAAGGT | 9420  |
| GCTCTCTGGC | GAGGTGGGCC | CGCAGGATGT | GCGGATCTCC | CGCCAGACCC | TTGAGTACCA | 9480  |
| GGCGCAGATT | GCCGAGCAGA | TGCAGCGCCA | TGCGGTGGCG | CGCAATTTCC | GCCGCGCGGC | 9540  |
| GGAGCTTATC | GCCATTCTTG | ACGAGCGCAT | TCTGGCTATC | TATAACGCGC | TGCGCCCGTT | 9600  |
| CCGCTCCTCG | CAGGCGGAGC | TGCTGGCGAT | CGCCGACGAG | CTGGAGCACA | CCTGGCATGC | 9660  |
| GACAGTGAAT | GCCGCCTTTG | TCCGGGAGTC | GGCGGAAGTG | TATCAGCAGC | GGCATAAGCT | 9720  |
| GCGTAAAGGA | AGCTAAGCGG | AGGTCAGCAT | GCCGTTAATA | GCCGGGATTG | ATATCGGCAA | 9780  |
| CGCCACCACC | GAGGTGGCGC | TGGCGTCCGA | CTACCCGCAG | GCGAGGGCGT | TTGTTGCCAG | 9840  |
| CGGGATCGTC | GCGACGACGG | GCATGAAAGG | GACGCGGGAC | AATATCGCCG | GGACCCTCGC | 9900  |
| CGCGCTGGAG | CAGGCCCTGG | CGAAAACACC | GTGGTCGATG | AGCGATGTCT | CTCGCATCTA | 9960  |
| TCTTAACGAA | GCCGCGCCGG | TGATTGGCGA | TGTGGCGATG | GAGACCATCA | CCGAGACCAT | 10020 |
| TATCACCGAA | TCGACCATGA | TCGGTCATAA | CCCGCAGACG | CCGGGCGGGG | TGGGCGTTGG | 10080 |

|            |            |            |             |            |            |       |
|------------|------------|------------|-------------|------------|------------|-------|
| CGTGGGGACG | ACTATCGCCC | TCGGGCGGCT | GGCGACGCTG  | CCGGCGGCGC | AGTATGCCGA | 10140 |
| GGGGTGGATC | GTACTGATTG | ACGACGCCGT | CGATTTCTT   | GACGCCGTGT | GGTGGCTCAA | 10200 |
| TGAGGCGCTC | GACCGGGGGA | TCAACGTGGT | GGCGGCGATC  | CTCAAAAAGG | ACGACGGCGT | 10260 |
| GCTGGTGAAC | AACCGCCTGC | GTAAAACCTT | GCCGGTGGTG  | GATGAAGTGA | CGCTGCTGGA | 10320 |
| GCAGGTCCCC | GAGGGGGTAA | TGGCGGCGGT | GGAAGTGGCC  | GCGCCGGGCC | AGGTGGTGCG | 10380 |
| GATCCTGTCT | AATCCCTACG | GGATCGCCAC | CTTCTTCGGG  | CTAAGCCCGG | AAGAGACCCA | 10440 |
| GGCCATCGTC | CCCATCGCCC | GCGCCCTGAT | TGGCAACCGT  | TCCGCGGTGG | TGCTCAAGAC | 10500 |
| CCCGCAGGGG | GATGTGCAGT | CGCGGGTGAT | CCCGGCGGGC  | AACCTCTACA | TTAGCGGCGA | 10560 |
| AAAGCGCCGC | GGAGAGGCCG | ATGTCGCCGA | GGGCGCGGAA  | GCCATCATGC | AGGCGATGAG | 10620 |
| CGCCTGCGCT | CCGGTACGCG | ACATCCGCGG | CGAACC GGCG | ACCCACGCCG | GCGGCATGCT | 10680 |
| TGAGCGGGTG | CGCAAGGTAA | TGGCGTCCCT | GACCGGCCAT  | GAGATGAGCG | CGATATACAT | 10740 |
| CCAGGATCTG | CTGGCGGTGG | ATACGTTTAT | TCCGCGCAAG  | GTGCAGGGCG | GGATGGCCGG | 10800 |
| CGAGTGCGCC | ATGGAGAATG | CCGTGCGGAT | GGCGGCGATG  | GTGAAAGCGG | ATCGTCTGCA | 10860 |
| AATGCAGGTT | ATCGCCCGCG | AACTGAGCGC | CCGACTGCAG  | ACCGAGGTGG | TGGTGGGCGG | 10920 |
| CGTGGAGGCC | AACATGGCCA | TCGCCGGGGC | GTTAACCCTT  | CCCGGCTGTG | CGGCGCCGCT | 10980 |
| GGCGATCCTC | GACCTCGGCG | CCGGCTCGAC | GGATGCGGCG  | ATCGTCAACG | CGGAGGGGCA | 11040 |
| GATAACGGCG | GTCCATCTCG | CCGGGGCGGG | GAATATGGTC  | AGCCTGTTGA | TTAAAACCGA | 11100 |
| GCTGGGCCTC | GAGGATCTTT | CGCTGGCGGA | AGCGATAAAA  | AAATACCCGC | TGGCCAAAGT | 11160 |
| GGAAAGCCTG | TTCAGTATTC | GTCACGAGAA | TGGCGCGGTG  | GAGTTCTTTC | GGGAAGCCCT | 11220 |
| CAGCCCGGCG | GTGTTGCGCA | AAGTGGTGTA | CATCAAGGAG  | GGCGAACTGG | TGCCGATCGA | 11280 |
| TAACGCCAGC | CCGCTGGAAA | AAATTCGTCT | CGTGCGCCGG  | CAGGCGAAAG | AGAAAGTGTT | 11340 |
| TGTCACCAAC | TGCCTGCGCG | CGCTGCGCCA | GGTCTCACCC  | GGCGGTTCCT | TTCGCGATAT | 11400 |
| CGCCTTTGTG | GTGCTGGTGG | GCGGCTCATC | GCTGGACTTT  | GAGATCCCGC | AGCTTATCAC | 11460 |
| GGAAGCCTTG | TCGCACTATG | GCGTGGTTCG | CGGGCAGGGC  | AATATTCGGG | GAACAGAAGG | 11520 |
| GCCGCGCAAT | GCGGTGCGCA | CCGGGCTGCT | ACTGGCCGGT  | CAGGCGAATT | AAACGGGCGC | 11580 |
| TCGCGCCAGC | CTCTCTCTTT | AACGTGCTAT | TTCAGGATGC  | CGATAATGAA | CCAGACTTCT | 11640 |
| ACCTTAACCG | GGCAGTGCGT | GGCCGAGTTT | CTTGGCACCG  | GATTGCTCAT | TTTCTTCGGC | 11700 |
| GCGGGCTGCG | TCGCTGCGCT | GCGGGTCCGC | GGGGCCAGCT  | TTGGTCAGTG | GGAGATCAGT | 11760 |
| ATTATCTGGG | GCCTTGCGGT | CGCCATGGCC | ATCTACCTGA  | CGGCCGGTGT | CTCCGGCGCG | 11820 |



|  |       |
|--|-------|
| CACCTAAATC CGGCGGTGAC CATTGCCCTG TGGCTGTTCTG CCTGTTTTGA ACGCCGCAAG | 11880 |
| GTGCTGCCGT TTATTGTTGC CCAGACGGCC GGGGCCTTCT GCGCCGCCGC GCTGGTGTAT  | 11940 |
| GGGCTCTATC GCCAGCTGTT TCTCGATCTT GAACAGAGTC AGCATATCGT GCGCGGCACT  | 12000 |
| GCCGCCAGTC TTAACCTGGC CGGGGTCTTT TCCACGTACC CGCATCCACA TATCACTTTT  | 12060 |
| ATACAAGCGT TTGCCGTGGA GACCACCATC ACGGCAATCC TGATGGCGAT GATCATGGCC  | 12120 |
| CTGACCGACG ACGGCAACGG AATTC  | 12145 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|                                 |    |
|---------------------------------|----|
| GGGAATTCAT GAAAAGATCA AAACGATTG | 30 |
|---------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|                                 |    |
|---------------------------------|----|
| GCGAATTCTT ATTCAATGGT GTCGGGCTG | 29 |
|---------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|                                  |    |
|----------------------------------|----|
| GCGAATTCAT GCAACAGACA ACCCAAATTC | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGAATTCAC TCCCTTACTA AGTCG

25

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGAATTCAT GAGCTATCGT ATGTTTG

27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGAATTCAG AATGCCTGGC GGAAAATC

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGAATTCAT GAGCGAGAAA ACCATGCG

28

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGAATTCTT AGCTTCCTTT ACGCAGC 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCTTAGGAG TCTAGAATAT TGAGCTCGAA TTCCCGGGCA TCGGTACCG GATCCAGAAA 60

AAAGCCCGCA CCTGACAGTG CGGGCTTTTT TTTT 94

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCAAGCTT AAGGAGGTTA ATTAAATGAA AAG 33

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTCTAGATT ATTCAATGGT GTCGGG 26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGCCGTCTA GAATTATGAG CTATCGTATG TTTGATTATC TG 42

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTGATACGG GATCCTCAGA ATGCCTGGCG GAAAAAT 36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGATCTGTGC TGTTTGCCAC GGTATGCAGC ACCAGCGCGA GATTATGGGC TCGCACGCTC 60

GACTGTCGGA CGGGGGCACT GGAACGAGAA GTCAGGCGAG CCGTCACGCC CTTGACAATG 120

CCACATCCTG AGCAAATAAT TCAACCACTA AACAAATCAA CCGCGTTTCC CGGAGGTAAC 180

C 181

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGATCTGTGC TGTTTGCCAC GGTATGCAGC ACCAGCGCGA GATTATGGGC TCGCACGCTC 60

GACTGTCGGA CGGGGGCACT GGAACATGCC ACATCCTGAG CAAATAATTC AACCACTAAA 120

CAAATCAACC GCGTTTCCCG GAGGTAACC

149

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGAATTCACT AGTCGATCTG TGCTGTTTGC CAC

33

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGGAAGCTT GGTTACCTCC GGGAAACGCG GTT

33

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGACCACAA GGAGGA

16

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAGTCCTCC TTGTGG

16

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTGGCCGTC GTTTTACTCG AGTCGTGACT GGGAAAACCC TGGCG

45

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATTCAAAGG AGGT

14

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTAGACCTCC TTTG

14

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGCTTGTCGA CCATGAAAA

19

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATCTTTTCA TGGTCGACA

19

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCGACCAGGA GGA

13

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTAGTCCTCC TGG

13

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCGACGAATT CAGGAGGA

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTAGTCCTCC TGAATTCG

18

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGTACAAGA TCCTGATCGC CGA

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCAGCGGCGC AGGTAGGCGG CG

22

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGACCAAGG GCCGGATCCG TCGACCTGCA G

31



(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTACCCTTGG CCCCGGATCC GTCGACCTGC AG

32

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CACGGCCTGG CGCAGGTTGC GGG

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCAGCCCGC ACGATTGCGG C

21

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGAAAACC GCCTGGATCG C

21

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGTTTCAGGG ACTGCAAAAC G

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAATTCAGA TCTCAGCAAT GAAAAGATCA AAACG

35

(2) INFORMATION FOR SEQ ID NO:39:

- (I) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGAATTCAGA TCTCAGCAAT GCAACAGACA ACCC

34

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GCTCTAGATC ACTCCCCCTTA CTAAGTCG

28

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGAATTCAGA TCTCAGCAAT GAGCGAGAAA ACCATGC

37

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCTCTAGATT AGCTTCCTTT ACGCAGC

27

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGAATTCAGA TCTCAGCAAT GAGCTATCGT ATGTTTGA

38

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCTCTAGATC AGAATGCCTG GCGG

24

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAATTCAGA TCTAGCAATG CCGTTAATAG CCGGG

35

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTCTAGATT AATTCGCCTG ACCGGC

26